

FIG. 1A Structural motifs in GRBP2

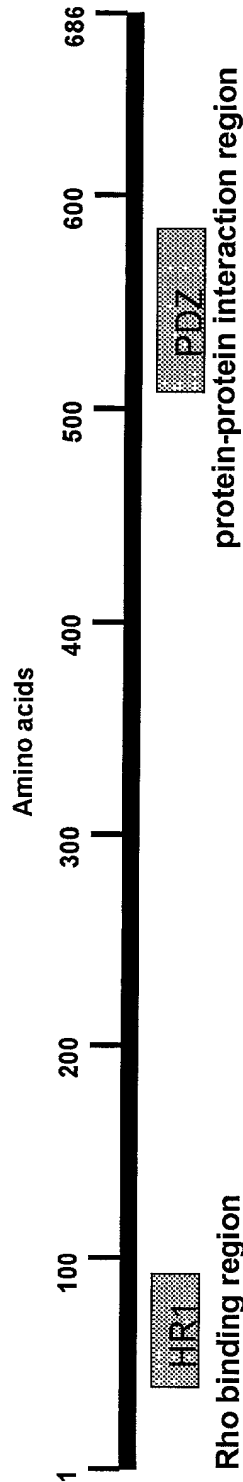


Fig. 1B HR1 domains

consensus	1	10	20	30	40	50	60
GRBP2	1	LLLELRKKLEVE	10	20	30	40	50
gi 7503594	38	nqraalnqqil	48	58	68	78	88
gi 6093970	159	sklivilqlf	169	179	189	199	209
gi 543444	42	shrarlhqq	52	62	72	82	92
gi 6319363	216	lrteelrhhf	226	236	246	256	266
gi 6225859	5	qlfqnirkk	15	25	35	45	55
gi 1085218	42	verdrirke	52	62	72	82	92
gi 1175418	38	klleedlkg	48	58	68	78	88

consensus	53	63
GRBP2	88	98
gi 7503594	210	220
gi 6093970	92	102
gi 543444	271	282
gi 6319363	55	65
gi 6225859	97	107
gi 1085218	92	102
gi 1175418	98	108

Fig. 1C PDZ domains

	10	20	30	40	50	60
consensus*.....*.....*.....*.....					
GRBP2	1 EPRLVELEKGG-----GGLGFSLVGKDSGD-----GGVVS SVVPGSPAAG- 44					
gi 13096475	513 PPRSIRFTAE-----GDLGFTLRGNA-----PVQVHFLDPYCSASVAG- 551					
gi 7512038	70 PSRLAALRRGTagvTGVGLEITIDGSG-----KDVVLTAPAGGPAEKAG- 116					
gi 6671754	405 EPRFISFQKE-----GSVGIRLTGGN-----eAGIFVTAVQPGSPASLQG- 444					
gi 7662086	484 EPTVEIIRLS-----DALGISIAGGKGSPlg-----dIPFIAMIQANGVAARTQK 531					
gi 131530	44 VQRCVIIQKQ-----HGFGFTVSGD-----RVLVQSVRPPGGAAMKAG- 82					
gi 6093970	507 YLVLRITPDe-----dGKFGFNKGEVDq-----kMPLVSRINPE SPADTCIp 551					
gi 7499828	497 LVGPVHMRGE-----GGFGFTLRGD-----SPVLIAAVVPGGQAE SAG- 535					
gi 8247939	46 RPHVVKVKSE-----TGFGFNKGVSEGGqlrslngqlyaPLQHVSAVLRRGADQAG- 100					
	410 IHVTILHKEEG-----AGLGFSLAGGADLEn-----KVITVHRVFPNGLASQEGT 454					
	70	80	90	100		
consensus*.....*.....*.....*.....					
GRBP2	45 -LKPEDVILEVNG-TSVEGLTHLEAVDLKE-AGG-----KVTLTLVLRGG 86					
gi 13096475	552 -AREGDYIVSIQL-VDCKWLTLEVMKLIKsfGED-----EIEMKVVSll 594					
gi 7512038	117 -ARAGDVIVTDG-TAVKGLSLYDVSDLIQG-EADs---QVEVVIHAPG 159					
gi 6671754	445 -LMPGDKILKVN-DMDNGVTRAEAVLFLLS-LQD-----RIDLIVQYCK 486					
gi 7662086	532 -LKVGDRIVSING-QPLDGLSHTDVAVNLLKN-AFG-----RIILQVADT 573					
gi 131530	83 -VREGDRIIKVNGtMVTNss-HLEVVKLIKsg-----aYVALTILGSS 123					
gi 6093970	552 KINEGDQIVLINGr-DISEHTDQVVMFika-SREshsrELALVIRRRRA 598					
gi 7499828	536 -LKEGDYIVSNG-QPCKWKKHLEWVTQIRs-MGEe---GVSLQVVSLL 578					
gi 8247939	101 -LRKGDRIILEVNG-LNVEGSTHRKVVVDLIKN-GGD-----ELTMIVISVE 142					
	455 -IQKNEVLSING-KSLKGTTHDAIAILRQ-AREp---RQAVIVTRKl 497					

FIG. 2
Genomic structure of human GRBP2

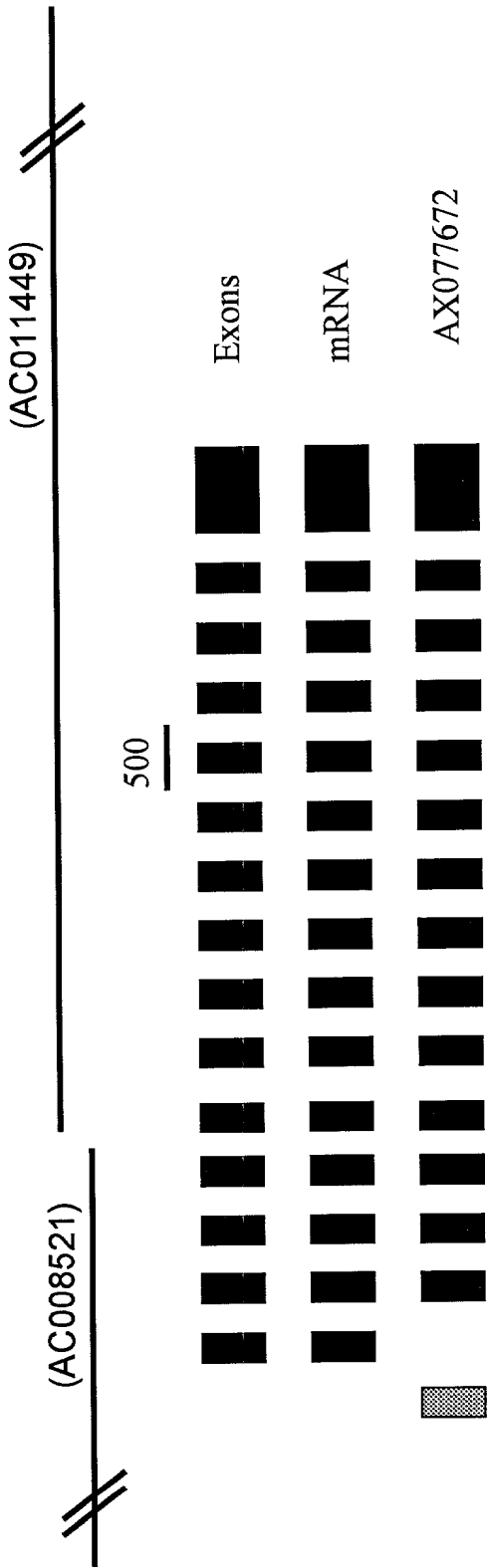


Fig. 3

Nucleotide and protein sequence of the GRBP2 gene

nt: SEQ ID NO: 1

aa: SEQ ID NO: 3

							M	T	D	A	L	L	6
tc	cgc	gcc	cgc	gcc	gct	agc	ATG	ACC	GAC	GCG	CTG	TTG	38
P	A	A	P	Q	P	L	E	K	E	N	D	G	19
CCC	GCG	GCC	CCC	CAG	CCG	CTG	GAG	AAG	GAG	AAC	GAC	GGC	77
Y	F	R	K	G	C	N	P	L	A	Q	T	G	32
TAC	TTT	CGG	AAG	GGC	TGT	AAT	CCC	CTT	GCA	CAA	ACC	GGC	116
R	S	K	L	Q	N	Q	R	A	A	L	N	Q	45
CGG	AGT	AAA	TTG	CAG	AAT	CAA	AGA	GCT	GCT	TTG	AAT	CAG	155
Q	I	L	K	A	V	R	M	R	I	G	A	E	58
CAG	ATC	CTG	AAA	GCC	GTG	CGG	ATG	AGG	ATC	GGA	GCG	GAA	194
N	L	L	K	V	A	T	N	S	K	V	R	E	71
AAC	CTT	CTG	AAA	GTG	GCC	ACA	AAC	TCA	AAG	GTG	CGG	GAG	233
Q	V	R	L	E	L	S	F	V	N	S	D	L	84
CAA	GTG	CGG	CTG	GAG	CTG	AGC	TTC	GTC	AAC	TCA	GAC	CTG	272
Q	M	L	K	E	E	L	E	G	L	N	I	S	97
CAG	ATG	CTC	AAG	GAA	GAG	CTG	GAG	GGG	CTG	AAC	ATC	TCG	311
V	G	V	Y	Q	N	T	E	E	A	F	T	I	110
GTG	GGC	GTC	TAT	CAG	AAC	ACA	GAG	GAG	GCA	TTT	ACG	ATT	350
P	L	I	P	L	G	L	K	E	T	K	D	V	124
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D	F	A	V	V	L	K	D	F	I	L	E	H	137
GAC	TTT	GCA	GTC	GTC	CTC	AAG	GAT	TTT	ATC	CTG	GAA	CAT	428
Y	S	E	D	G	Y	L	Y	E	D	E	I	A	150
TAC	AGT	GAA	GAT	GGC	TAT	TTA	TAT	GAA	GAT	GAA	ATT	GCA	467
D	L	M	D	L	R	Q	A	C	R	T	P	S	163
GAT	CTT	ATG	GAT	CTG	AGA	CAA	GCT	TGT	CGG	ACG	CCT	AGC	506

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ATC	CAG	CTG	GGC	TTT	GTC	GAG	AGT	CGA	TTC	TTC	CCG	CCC	584
T	R	Q	M	G	L	L	F	T	W	Y	D	S	201
ACA	CGG	CAG	ATG	GGA	CTC	CTG	TTC	ACC	TGG	TAT	GAC	TCT	623
L	T	G	V	P	V	S	Q	Q	N	L	L	L	214
CTC	ACC	GGG	GTT	CCG	GTC	AGC	CAG	CAG	AAC	CTG	CTG	CTG	662
E	K	A	S	V	L	F	N	T	G	A	L	Y	227
GAG	AAG	GCC	AGT	GTC	CTG	TTC	AAC	ACT	GGG	GCC	CTC	TAC	701
T	Q	I	G	T	R	C	D	R	Q	T	Q	A	240
ACC	CAG	ATT	GGG	ACC	CGG	TGC	GAT	CGG	CAG	ACG	CAG	GCT	740
G	L	E	S	A	I	D	A	F	Q	R	A	A	253
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G	V	L	N	Y	L	K	D	T	F	T	H	T	266
GGG	GTT	TTA	AAT	TAC	CTG	AAA	GAC	ACA	TTT	ACC	CAT	ACT	818
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CCA	AGT	TAC	GAC	ATG	AGC	CCT	GCC	ATG	CTC	AGC	GTG	CTC	857
V	K	M	M	L	A	Q	A	Q	E	S	V	F	292
GTC	AAA	ATG	ATG	CTT	GCA	CAA	GCC	CAA	GAA	AGC	GTG	TTT	896
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GAG	GTC	TAC	CAA	CAG	CTA	CAC	GCA	GCC	ATG	AGC	CAG	GCG	1013
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CCG	GTG	AAA	GAG	AAC	ATC	CCC	TAC	TCC	TGG	GCC	AGC	TTA	1052
A	C	V	K	A	H	H	Y	A	A	L	A	H	357
GCC	TGC	GTG	AAG	GCC	CAC	CAC	TAC	GCG	GCC	CTG	GCC	CAC	1091
Y	F	T	A	I	L	L	I	D	H	Q	V	K	370
TAC	TTC	ACT	GCC	ATC	CTC	CTC	ATC	GAC	CAC	CAG	GTG	AAG	1130

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CAG	CTC	TAC	GAC	CAC	ATG	CCA	GAG	GGG	CTG	ACA	CCC	TTG	1208
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GCC	ACA	CTG	AAG	AAT	GAT	CAG	CAG	CGC	CGA	CAG	CTG	GGG	1247
K	S	H	L	R	R	A	M	A	H	H	E	E	422
AAG	TCC	CAC	TTG	CGC	AGA	GCC	ATG	GCT	CAT	CAC	GAG	GAG	1286
S	V	R	E	A	S	L	C	K	K	L	R	S	435
TCG	GTG	CGG	GAG	GCA	AGC	CTC	TGC	AAG	AAG	CTG	CGG	AGC	1325
I	E	V	L	Q	K	V	L	C	A	A	Q	E	448
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AAA	ACT	GAG	CAA	GAG	GTT	GAC	ATT	ATA	TTG	CCC	CAG	TTC	1481
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TCC	AAG	CTG	ACA	GTC	ACG	GAC	TTC	TTC	CAG	AAG	CTG	GGC	1520
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CCC	TTA	TCT	GTG	TTT	TCG	GCT	AAC	AAG	CGG	TGG	ACG	CCT	1559
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CCT	CGA	AGC	ATC	CGC	TTC	ACT	GCA	GAA	GAA	GGG	GAC	TTG	1598
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TTC	CTG	GAT	CCT	TAC	TGC	TCT	GCC	TCG	GTG	GCA	GGA	GCC	1676
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CGG	GAA	GGA	GAT	TAT	ATT	GTC	TCC	ATT	CAG	CTT	GTG	GAT	1715
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 cac cac aac cgt ccc act att tta ctt ttt aaa atg aca 3236
 ttc cta ctg att gat ttt tat ctt gct ata agt tcg atg 3275
 aca ccg tga atc taa taa ggt tca ctg ttg aca cag tac 3314
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